

sequences, SEQ ID NOs:1-38, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.

This amendment contains no new matter. The amendments to the specification and claims introducing sequence ID numbers simply provide appropriate cross-reference from the sequences in the application to the formal sequence listing. Replacement Figures 5 and 6 also introduce no new matter. The letters that are now visible in the "POINTED/A-REGION" and the "ETS-DNA Binding Domain" can be determined by reference to Figure 4 and to SEQ ID NO 15 as filed. The corrections to the mESX sequence in Figures 5 and 6 can be determined by reference to the mESX sequence in the Sequence Listing as filed. Moreover, it is noted that the specification teaches that Applicants isolated and sequenced the human and mouse ESX genes. The corrections to Figures 5 and 6 simply reflect the correct polypeptide sequence and as such, are inherent in the isolated nucleic acids (*see, e.g., Kennecott Corp. v Kyocera Internat., Inc. and Kyoto Ceramic Co., Ltd.* 5 USPQ2d 1194 (Fed. Cir. 1987))

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at (415) 576-0200.

Respectfully submitted,



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ESX Primary Structure and Domain Homologies.

mESX	1 MAATCEISNVFSNYFNAMYSSEDPTLAPAPP . TTFGTEDLVTLNNQQMT	49
	: . : . .	
hESX	1 MAATCEISNIFSNYFSAMYSSEDSTLASVPPAATFGADDLVLTLSNPQMS	50
	E_1/E_2 ↓	
mESX	50 LEGPEKASWTSERPQFWSKTQVLEWISYQVEKNKYDASSIDFSRCNMDGA	99
	: . : . .	
hESX	51 LEGTEKASWLGEQPQFWSKTQVLDWISYQVEKNKYDASAIDFSRCDMGDA	100
	E_1/E_2 ↓	
mESX	100 TLCSCALEELRLVFGPLGDQLHAQLRDLTSNSSDELSWIIELLEDGMSF	149
	: 	
hESX	101 TLCNCALEELRLVFGPLGDQLHAQLRDLTSSSSDELSWIIELLEDGMAF	150
	E_1/E_2 ↓	E_1/E_2 ↓
mESX	150 QESLGDLGP S DQGSPFAQELLDDGRQASPYYCSTYPGAPSPGSSDVSTA	199
	. : 	
hESX	151 QEAL.DPGPF D QGSPFAQELLDDGQQASPYHPGSCGAGAPSPGSSDVSTA	199
	E_1/E_2 ↓	
mESX	200 G TATPQSSHASDGGSDVDLDTESKVFRDDFTDYKKGEPKHGKRKGR	249
	. : 	
hESX	200 GTGASRSSHSSDGGSDVDLDP T DGKL F PSDGFRDCKKGDPKHGKRKGR	249
	E_1/E_2 ↓	
mESX	250 PRKLSKEYWDCLEGKKS K HAPRG T	299
	: 	
hESX	250 PRKLSKEYWDCLEGKKS K HAPRG T	299
	E_1/E_2 ↓	
mESX	300 EG V KE R SEAVAV L W C RR K RSN	349
	: 	
hESX	300 EG V KE R SEAVAV L W C RR K RSN	349
mESX	350 WAK GKNSSGWKEEEVGESRN	371
	: 	
hESX	350 WAK GKNSSGWKEEEVLQSRN	371

— POINTED / A-Region
■ Serine-Rich Box
■ Nuclear Targeting Sequence
■ ETS-DNA Binding Domain

Conserved Elements in ESX Proximal Promoter.

mESX -347 TCAGCCCTGGCCAGGCCCCCAGGAAGAATTTCAGGGCCAGAGGGCAGCC -298
 hESX -350 CCATCTCTGGCTGGCCCTGGGAGGAATTCCCTGGGCCAGAGGGCAGCC -301

mESX -297 TAAGGCACAGATGCCAACCCCTGCAATGTTCCCGCCACGTGCCAGTTCA -246
 hESX -300 GAAAGCACAGATGCCAACCCAGCAACGTTCCCGCCACCTGCCAGGCCA -251

mESX -247 GTACCCAGGGCCAACCCCAGAGGGTGGGAATGACAGATTCTGACAATC -198
 hESX -250 GTGCCCGTGCCCAACCCCAGAGGGTGGGGATGACAGACTCTGACAATC -201

mESX -197 ATTAAACCAGCCAGGCCTGATTCCCAGCACCGCCGTAGGATGTGGC -146
 hESX -200 ATTAAACCAGCCGGGCTGATTCCCAGCACTGCCCTGCTAAGATCCGGC -151

mESX -147 CAAGTGGCACCGAATATGCAAATCACGTGGACAGGGAGCCCAGTCTGAA -98
 hESX -150 CAAGTGGCACTGAATATGCAAATCACCTGGGCCAGGAGCCCAGTCTAAA -101

mESX -97 GGCCAGGAAATCCCCAGCATCCAATGAGCCACCAGCTCAGGTTACAACCG -46
 hESX -100 GGCCAGGAAATCCCCATCCAATGAGACACCAGCTCAGGTTACTGCAG -49

mESX -47 GGGACGTACGCCGAAGACCTG...GAGGGGAGGAGCTCTGCTTGCTCT -1
 hESX -50 GGGACACACTATAAGCCCTGAGCTCAGGGAGGAGCTCCCTCAGGCTCT -1

mESX +1 ATTTAGAGCGGGTGGGGCAGCGCCCTGGCCACACTCATCACTGCTACCT +50
 hESX +1 ATTTAGAGCGGGTAGGGAGGCCAGCAGATACCTCAGCGCTACCT +50

Ets	USF
AP-2	Oct
extended palindrome	NF-κB
SP1/GC box	CCAAT box & Inn element

Fig. 6